

MAP8 Rec'd PCT/PTO 02 DEC 2005  
SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
HUMAN SERVICES

Schneerson, Rachel  
Leppla, Stephen H.  
Robbins, John B.  
Shiloach, Joseph  
Kubler-Kielb, Joanna  
Liu, Darrell  
Majadly, Fathy

<120> GAMMA PGA CONJUGATES FOR ELICITING IMMUNE RESPONSES DIRECTED  
AGAINST BACILLI

<130> 4239-68226-01

<150> US 60/476,598

<151> 2003-06-05

<160> 3

<170> PatentIn version 3.2

<210> 1

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Basic peptide derived from HIV-1 Tat protein.

<400> 1

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln  
1 5 10

<210> 2

<211> 2295

<212> DNA

<213> Bacillus anthracis

<220>

<221> CDS

<222> (1)..(2292)

<400> 2

atg aaa aaa cga aaa gtg tta ata cca tta atg gca ttg tct acg ata  
Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile  
1 5 10 15

48

tta gtt tca agc aca ggt aat tta gag gtg att cag gca gaa gtt aaa  
Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys  
20 25 30

96

cag gag aac cgg tta aat gaa tca gaa tca agt tcc cag ggg tta  
Gln Glu Asn Arg Leu Leu Asn Glu Ser Ser Ser Gln Gly Leu

144

35	40	45	
ctt gga tac tat ttt agt gat ttg aat ttt caa gca ccc atg gtg gtt Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val	50	55	192
		60	
acc tct tct act aca ggg gat tta tct att cct agt tct gag tta gaa Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu	65	70	240
		75	
		80	
aat att cca tcg gaa aac caa tat ttt caa tct gct att tgg tca gga Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly	85	90	288
		95	
ttt atc aaa gtt aag aag agt gat gaa tat aca ttt gct act tcc gct Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala	100	105	336
		110	
gat aat cat gta aca atg tgg gta gat gac caa gaa gtg att aat aaa Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys	115	120	384
		125	
gct tct aat tct aac aaa atc aga tta gaa aaa gga aga tta tat caa Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln	130	135	432
		140	
ata aaa att caa tat caa cga gaa aat cct act gaa aaa gga ttg gat Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp	145	150	480
		155	
		160	
ttc aag ttg tac tgg acc gat tct caa aat aaa aaa gaa gtg att tct Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser	165	170	528
		175	
agt gat aac tta caa ttg cca gaa tta aaa caa aaa tct tcg aac tca Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser	180	185	576
		190	
aga aaa aag cga agt aca agt gct gga cct acg gtt cca gac cgt gac Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp	195	200	624
		205	
aat gat gga atc cct gat tca tta gag gta gaa gga tat acg gtt gat Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp	210	215	672
		220	
gtc aaa aat aaa aga act ttt ctt tca cca tgg att tct aat att cat Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His	225	230	720
		235	
		240	
gaa aag aaa gga tta acc aaa tat aaa tca tct cct gaa aaa tgg agc Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser	245	250	768
		255	
acg gct tct gat ccg tac agt gat ttc gaa aag gtt aca gga cgg att Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile	260	265	816
		270	
gat aag aat gta tca cca gag gca aga cac ccc ctt gtg gca gct tat Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr			864

275

280

285

ccg att gta cat gta gat atg gag aat att att ctc tca aaa aat gag 912  
 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu  
 290 295 300

gat caa tcc aca cag aat act gat agt caa acg aga aca ata agt aaa 960  
 Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys  
 305 310 315 320

aat act tct aca agt agg aca cat act agt gaa gta cat gga aat gca 1008  
 Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala  
 325 330 335

gaa gtg cat gcg tcg ttc ttt gat att ggt ggg agt gta tct gca gga 1056  
 Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly  
 340 345 350

ttt agt aat tcg aat tca agt acg gtc gca att gat cat tca cta tct 1104  
 Phe Ser Asn Ser Asn Ser Thr Val Ala Ile Asp His Ser Leu Ser  
 355 360 365

cta gca ggg gaa aga act tgg gct gaa aca atg ggt tta aat acc gct 1152  
 Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala  
 370 375 380

gat aca gca aga tta aat gcc aat att aga tat gta aat act ggg acg 1200  
 Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr  
 385 390 395 400

gct cca atc tac aac gtg tta cca acg act tcg tta gtg tta gga aaa 1248  
 Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys  
 405 410 415

aat caa aca ctc gcg aca att aaa gct aag gaa aac caa tta agt caa 1296  
 Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln  
 420 425 430

ata ctt gca cct aat aat tat tat cct tct aaa aac ttg gcg cca atc 1344  
 Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile  
 435 440 445

gca tta aat gca caa gac gat ttc agt tct act cca att aca atg aat 1392  
 Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn  
 450 455 460

tac aat caa ttt ctt gag tta gaa aaa acg aaa caa tta aga tta gat 1440  
 Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp  
 465 470 475 480

acg gat caa gta tat ggg aat ata gca aca tac aat ttt gaa aat gga 1488  
 Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly  
 485 490 495

aga gtg agg gtg gat aca ggc tcg aac tgg agt gaa gtg tta ccg caa 1536  
 Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln  
 500 505 510

att caa gaa aca act gca cgt atc att ttt aat gga aaa gat tta aat 1584  
 Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn

515	520	525	
ctg gta gaa agg cgg ata gcg gcg gtt aat cct agt gat cca tta gaa Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu			1632
530	535	540	
acg act aaa ccg gat atg aca tta aaa gaa gcc ctt aaa ata gca ttt Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe			1680
545	550	555	560
gga ttt aac gaa ccg aat gga aac tta caa tat caa ggg aaa gac ata Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile			1728
565	570	575	
acc gaa ttt gat ttt aat ttc gat caa caa aca tct caa aat atc aag Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys			1776
580	585	590	
aat cag tta gcg gaa tta aac gca act aac ata tat act gta tta gat Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp			1824
595	600	605	
aaa atc aaa tta aat gca aaa atg aat att tta ata aga gat aaa cgt Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg			1872
610	615	620	
ttt cat tat gat aga aat aac ata gca gtt ggg gcg gat gag tca gta Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val			1920
625	630	635	640
gtt aag gag gct cat aga gaa gta att aat tcg tca aca gag gga tta Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu			1968
645	650	655	
ttg tta aat att gat aag gat ata aga aaa ata tta tca ggt tat att Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile			2016
660	665	670	
gta gaa att gaa gat act gaa ggg ctt aaa gaa gtt ata aat gac aga Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg			2064
675	680	685	
tat gat atg ttg aat att tct agt tta cgg caa gat gga aaa aca ttt Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe			2112
690	695	700	
ata gat ttt aaa aaa tat aat gat aaa tta ccg tta tat ata agt aat Ile Asp Phe Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn			2160
705	710	715	720
ccc aat tat aag gta aat gta tat gct gtt act aaa gaa aac act att Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile			2208
725	730	735	
att aat cct agt gag aat ggg gat act agt acc aac ggg atc aag aaa Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys			2256
740	745	750	
att tta atc ttt tct aaa aaa ggc tat gag ata gga taa Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly			2295

755

760

<210> 3  
<211> 764  
<212> PRT  
<213> *Bacillus anthracis*  
  
<400> 3

Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile  
1 5 10 15

Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys  
20 25 30

Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Gln Gly Leu  
35 40 45

Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val  
50 55 60

Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu  
65 70 75 80

Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly  
85 90 95

Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala  
100 105 110

Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys  
115 120 125

Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln  
130 135 140

Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp  
145 150 155 160

Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser  
165 170 175

Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser  
180 185 190

Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp  
195 200 205

Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp  
210 215 220

Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His  
225 230 235 240

Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser  
245 250 255

Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile  
260 265 270

Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr  
275 280 285

Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu  
290 295 300

Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys  
305 310 315 320

Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala  
325 330 335

Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly  
340 345 350

Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser  
355 360 365

Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala  
370 375 380

Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr  
385 390 395 400

Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys  
405 410 415

Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln  
420 425 430

Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile  
435 440 445

Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn  
450 455 460

Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp  
465 470 475 480

Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly  
485 490 495

Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln  
500 505 510

Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn  
515 520 525

Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu  
530 535 540

Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe  
545 550 555 560

Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile  
565 570 575

Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys  
580 585 590

Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp  
595 600 605

Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg  
610 615 620

Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val  
625 630 635 640

Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu  
645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile  
660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg  
675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe  
690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn  
705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile  
725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys  
740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly  
755 760